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FIGURE 1A

1	GCACGAGAACTTTGCTGTGCGCGTTCTCCCGCGCGGGCTCAACTTTGTAGAGCGAGG	60
61	GGCCAACTTGGCAGAGCGCGGCCAGCTTTGCAGAGAGCGCCCTCCAGGGACTATGCGT	120
121	GCGGGGACACGGGTGCGTTTGGGCTCTTCCACCCCTGCGGAGCGCACTACCCGAGCCAG	180
181	GGGCGGTGCAAGCCCCGCCGGCCCTACCCAGGGGGCTCCTCCCTCCGAGCGCCGAGA	240
241	CTTTTAGTTTCGCTTTTCGCTAAAGGGGCCCCAGACCCCTTGCTGCGGAGCGACGGAGAGAG	300
301	ACTGTGCCAGTCCCAGCGCCCTACCGCCGTGGGAACGATGGCAGATGATCAGGGCTGTA	360
1	M A D D Q G C I	8
361	TTGAAGAGCAGGGGGTTGAGGATTCAGCAAATGAAGATTCAGTGGATGCTAAGCCAGACC	420
9	E E Q G V E D S A N E D S V D A K P D R	28
421	GGTCCTCGTTTGTACCGTCCCTCTTCAGTAAGAAGAAGAAAATGTCACCATGCGATCCA	480
29	S S F V P S L F S K K K K N V T M R S I	48
481	TCAAGACCACCGGGACCGAGTGCCTACATATCAGTACAACATGAATTTTGAAAAGCTGG	540
49	K T T R D R V P T Y Q Y N M N F E K L G	68
541	GCAAATGCATCATAATAACAACAAGAACTTTGATAAAGTGACAGGTATGGGCGTTCGAA	600
69	K C I I I N N K N F D K V T G M G V R N	88
601	ACGGAACAGACAAAGATGCCGAGGCGCTCTTCAAGTGCTTCCGAAGCCTGGGTTTTGACG	660
89	G T D K D A E A L F K C F R S L G F D V	108
661	TGATTGTCTATAATGACTGCTCTTGTGCCAAGATGCAAGATCTGCTTAAAAAAGCTTCTG	720
109	I V Y N D C S C A K M Q D L L K K A S E	128
721	AAGAGGACCATACAAATGCCGCTGCTTGCCTGCATCCTCTTAAGCCATGGAGAAGAAA	780
129	E D H T N A A C F A C I L L S H G E E N	148
781	ATGTAATTTATGGGAAAGATGGTGTACACCAATAAAGGATTTGACAGCCCACTTTAGGG	840
149	V I Y G K D G V T P I K D L T A H F R G	168
841	GGGATAGATGCAAAACCCCTTTTAGAGAAACCCAAACTCTTCTTCATTTCAGGCTTGCCGAG	900
169	D R C K T L L E K P K L F F I Q A C R G	188
901	GGACCGAGCTTGATGATGCCATCCAGGCCGACTCGGGGGCCATCAATGACACAGATGCTA	960
189	T E L D D A I Q A D S G P I N D T D A N	208

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FIGURE 1B

961	ATCCTCGATACAAGATCCCAGTGGAGCTGACTTCCTCTTCGCCTATTCCACGGTTCCAG	1020
209	P R Y K I P V E A D F L F A Y S T V P G	228
1021	GCTATTACTCGTGGAGGAGCCCAGGAAGAGGCTCCTGGTTGTGCAAGCCCTCTGCTCCA	1080
229	Y Y S W R S P G R G S W F V Q A L C S I	248
1081	TCCTGGAGGAGCACGGAAAAGACCTGGAAATCATGCAGATCCTCACCAGGGTGAATGACA	1140
249	L E E H G K D L E I M Q I L T R V N D R	268
1141	GAGTTGCCAGGCACCTTTGAGTCTCAGTCTGATGACCCACACTTCCATGAGAAGAAGCAGA	1200
269	V A R H F E S Q S D D P H F H E K K Q I	288
1201	TCCCTGTGTGGTCTCCATGCTCACCAAGGAACCTCTACTTCAGTCAATAGCCATATCAGG	1260
289	P C V V S M L T K E L Y F S Q	303
1261	GGTACATTCTAGCTGAGAAGCAATGGGTCACTCATTAAATGAATCACATTTTTTTATGCTC	1320
1321	TTGAAATATTTCAGAAATTCTCCAGGATTTTAATTTTCAGGAAAATGTATT	1369

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FIGURE 2A

1 GCACGAGCGGATGGGTGCTATTGTGAGGCGGTTGTAGAAGAGTTTCGTGAGTGCTCGCAG 60
61 CTCATACCTGTGGCTGTGTATCCGTGGCCACAGCTGGTTGGCGTCGCCTTGAAATCCCAG 120
121 GCCGTGAGGAGTTAGCGAGCCCTGCTCACACTCGGCGCTCTGGTTTTCGGTGGGTGTGCC 180
181 CTGCACCTGCCTCTTCCCGCATTCTCATTAAATAAAGGTATCCATGGAGAACACTGAAAAC 240
1 M E N T E N 6
241 TCAGTGGATTCAAAATCCATTAAAAATTTGGAACCAAAGATCATACTGGAAGCGAATCA 300
7 S V D S K S I K N L E P K I I H G S E S 26
301 ATGGACTCTGGAATATCCCTGGACAACAGTTATAAAATGGATTATCCTGAGATGGGTTTA 360
27 M D S G I S L D N S Y K M D Y P E M G L 46
361 TGTATAATAATTAATAATAAGAATTTTCATAAAAGCACTGGAATGACATCTCGGTCTGGT 420
47 C I I I N N K N F H K S T G M T S R S G 66
421 ACAGATGTGATGCAGCAAACCTCAGGGAAACATTGAGAACTTGAAATATGAAGTCAGG 480
67 T D V D A A N L R E T F R N L K Y E V R 86
481 AATAAAAAATGATCTTACACGTGAAGAAATTGTGGAATTGATGCGTGATGTTTCTAAAGAA 540
87 N K N D L T R E E I V E L M R D V S K E 106
541 GATCACAGCAAAGGAGCAGTTTTGTTTGTGTGCTTCTGAGCCATGGTGAAGAAGGAATA 600
107 D H S K R S S F V C V L L S H G E E G I 126
601 ATTTTGGAAACAAATGGACCTGTTGACCTGAAAAAATAACAACTTTTTCAGAGGGGAT 660
127 I F G T N G P V D L K K I T N F F R G D 146
661 CGTTGTAGAAGTCTAACTGGAACCCAACTTTTCATTATTCAGGCCTGCCGTGGTACA 720
147 R C R S L T G K P K L F I I Q A C R G T 166
721 GAACTGGACTGTGGCATTGAGACAGACAGTGGTGTGATGATGACATGGCGTGTCATAAA 780
167 E L D C G I E T D S G V D D D M A C H K 186
781 ATACCAGTGGAGGCCGACTTCTTGATGCATACTCCACAGCACCTGGTTATTATTCTTGG 840
187 I P V E A D F L Y A Y S T A P G Y Y S W 206

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FIGURE 2B

841 CGAAATTCAAAGGATGGCTCCTGGTTTCATCCAGTCGCTTTGTGCCATGCTGAAACAGTAT 900
207 R N S K D G S W F I Q S L C A M L K Q Y 226

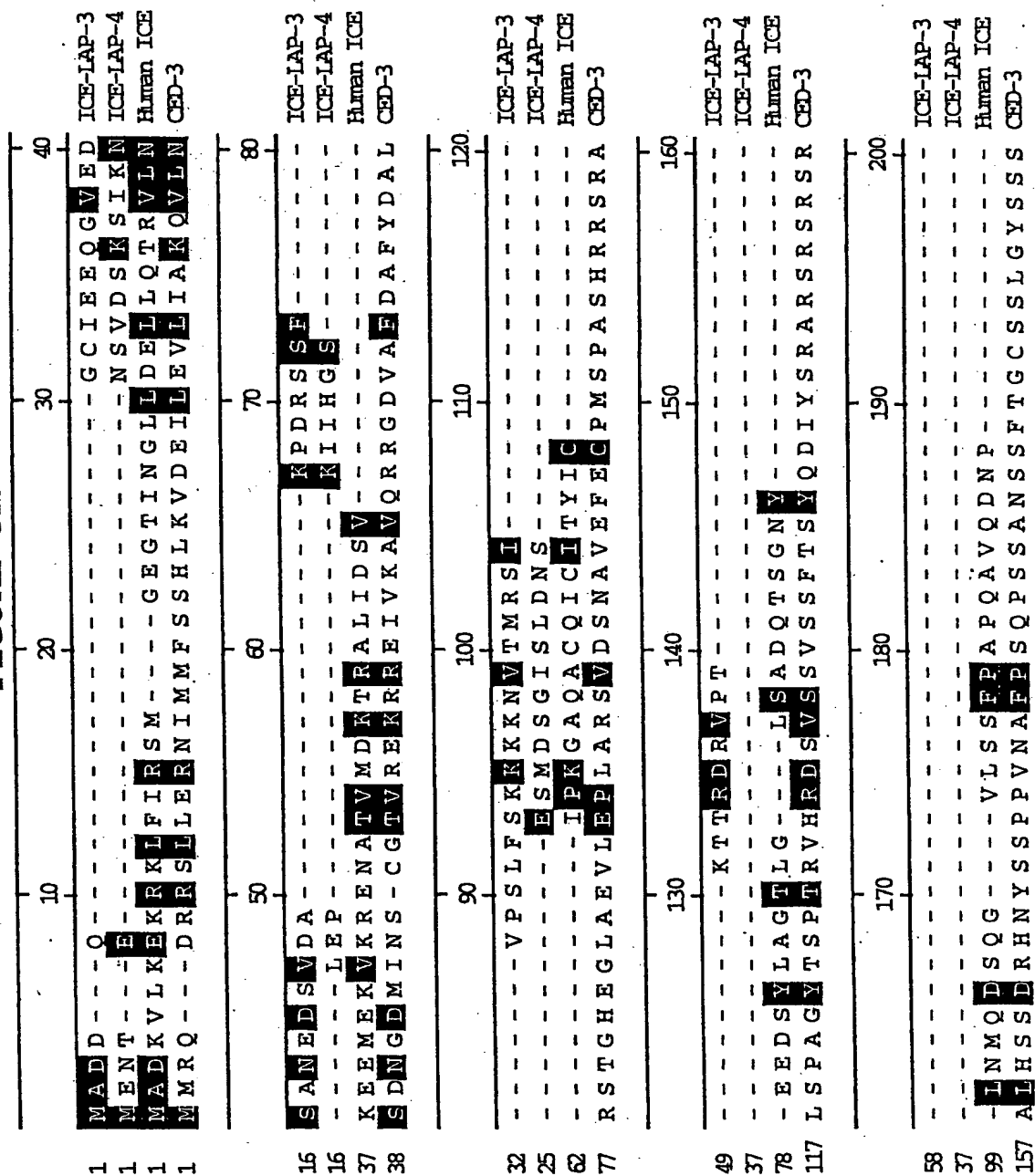
901 GCCGACAAGCTTGAATTTATGCACATTCTTACCCGGGTTAACCGAAAGGTGGCAACAGAA 960
227 A D K L E F M H I L T R V N R K V A T E 246

961 TTTGAGTCCTTTTCCTTTGACGCTACTTTTCATGCAAAGAAACAGATTCCATGTATTGTT 1020
247 F E S F S F D A T F H A K K Q I P C I V 266

1021 TCCATGCTCACAAAAGAACTCTATTTTTATCACTAAAGAAATGGTTGGTTGGTGGTTTTT 1080
267 S M L T K E L Y F Y H * 277

1081 TTTAGTTTGTATGCCAAGTGAGAAGATGGTATATTTGGGTACTGTATTTCCCTCTCATTG 1140

1141 GGGACCTACTCTCATGCTG 1159



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FIGURE 3B

	210	220	230	240	
58	-	-	-	-	ICE-LAP-3
37	-	-	-	-	ICE-LAP-4
122	-	-	-	-	Human ICE
197	-	-	-	-	CED-3
	250	260	270	280	
68	-	-	-	-	ICE-LAP-3
45	-	-	-	-	ICE-LAP-4
153	-	-	-	-	Human ICE
235	-	-	-	-	CED-3
	290	300	310	320	
98	-	-	-	-	ICE-LAP-3
75	-	-	-	-	ICE-LAP-4
190	-	-	-	-	Human ICE
270	-	-	-	-	CED-3
	330	340	350	360	
136	-	-	-	-	ICE-LAP-3
113	-	-	-	-	ICE-LAP-4
230	-	-	-	-	Human ICE
308	-	-	-	-	CED-3
	370	380	390	400	
170	-	-	-	-	ICE-LAP-3
147	-	-	-	-	ICE-LAP-4
269	-	-	-	-	Human ICE
342	-	-	-	-	CED-3

FIGURE 3C

[illegible]

Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.